

De Novo Balanced Translocation (6;18)(q21;q21.3) in a Patient With Heterotaxia

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We report on a sporadic case of heterotaxia with a de novo chromosome structural abnormality. The patient had inversely located heart (dextrocardia), stomach, duodenum, and cecum. In addition, she had cerebral atrophy, hypertelorism with telecanthus, infraorbital skin furrows, ear-lobe grooves, prominent maxilla and teeth, large carp mouth, short fifth fingers with limited flexion, generalized hypotonicity, and severe psychomotor retardation. High-resolution chromosome banding analysis demonstrated an apparently balanced translocation: 46,XX,t(6;18)(q21;q21.3). It is hypothesized that both heterotaxia and the chromosomal abnormality in the patient are causally related and a putative situs determining gene has been disrupted by the chromosome break, i.e., a position effect or a cryptic deletion at around the breakpoints. The translocation in our patient may be a good source for positional cloning of the gene.

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KEY WORDS: heterotaxia, translocation, 6q21, 18q21.3, situs determining gene, Iv, Inv, connexin43 gene

INTRODUCTION

Heterotaxia, a lateralization defect occurring in an early embryonic period, is characterized by inverse position of visceral organs frequently associated with chest and abdominal malformations, such as tetralogy of Fallot, transposition of great vessels, pulmonary valve stenosis, ventricular/atrial septal defect (ASD), and asplenia-polysplenia. Heterotaxia occurs approximately in one in 10,000 births. Although it is generally

accepted that lateralization, left-right asymmetry, of visceral organs is genetically determined, its mechanism has not been clarified. Several different inheritance modes have been proposed for familial heterotaxia: autosomal recessive [Arnold et al., 1983; Gatrads et al., 1984; Czeizel, 1987; Distefano et al., 1987; Zlotogora et al., 1987], autosomal dominant [Niikawa et al., 1983; Alonso et al., 1995], or X-linked recessive inheritance [Casey et al., 1993]. Different inheritance patterns suggest that multiple genes contribute to the determination of left-right asymmetry. Chromosome structural aberrations reported to be associated with heterotaxia may indicate the localization of the putative gene(s) for situs determination to the breakpoints: t(12;13)(q13.1;p13) [Wilson et al., 1991] and inv(11)(q13q25) [Fukushima et al., 1993]. Here we report another sporadic case of heterotaxia with a de novo balanced chromosome translocation.

CLINICAL REPORT

The female patient was born at 40 weeks of gestation with a birth weight of 3,090 g to non-consanguineous, phenotypically normal parents. The pregnancy and delivery are uneventful. At age 1 month, a pediatrician noted that her heart sounds were heard at the right fourth intercostal space and the liver was palpable 1 cm below the left costal margin. When seen by us at age 10 years, she weighed 22 kg (-2.0 SD) and measured 123 cm (-1.5 SD). She had generalized hypotonicity and severe psychomotor retardation; she could not stand up without support nor speak a word. Minor anomalies noted were as follows: hypertelorism with telecanthus, infraorbital skin furrows, ear-lobe grooves, prominent maxilla and teeth, large mouth (Fig. 1A), and short fifth fingers with limited flexion. A chest-abdominal roentgenogram showed dextrocardia and a gastric bubble in the right upper abdomen (Fig. 1B). Barium roentgenogram demonstrated a left stomach, reversely located duodenum and left cecum. Barium enema, scintigraphy, and catheter examinations were refused by the parents. Sleep records of electroencephalogram (EEG) were normal. Computerized tomography (CT) of the brain demonstrated cerebral atrophy. She had no history of recurrent infections suspected of splenic dysfunction. High-resolution chromosome banding analysis showed an apparently balanced translocation

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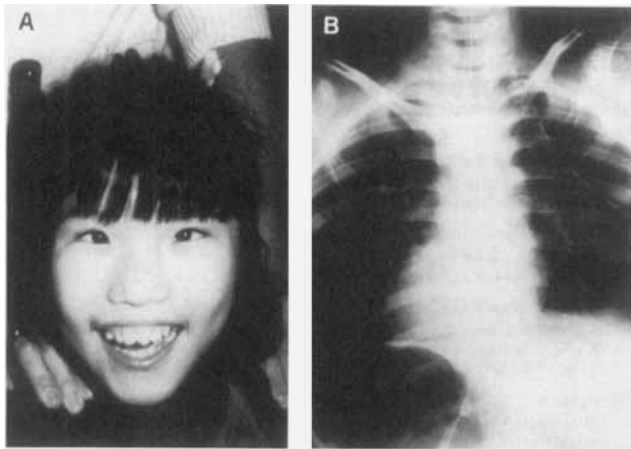


Fig. 1. Minor anomalies on the face (A), and dextrocardia and a gastric bubble in the right upper abdomen (B).

between 6q21 and 18q21.3 (Fig. 2). Karyotypes of her parents were normal. Thus, the karyotype of the patient was interpreted as 46,XX,t(6;18)(q21;q21.3) de novo.

DISCUSSION

The present case of heterotaxia was sporadic and her translocation a de novo type and balanced. It is a hypothesis that both the situs and chromosomal abnormalities are causally related and that a putative situs determining gene was disrupted by the break, i.e., a position effect or a cryptic deletion at around the breakpoints. Thus, the translocation in our patient may be a good source for positional cloning of the gene. Alternatively, in view of the presence of other phenotypic abnormalities, the chromosomal rearrangement was coincidental.

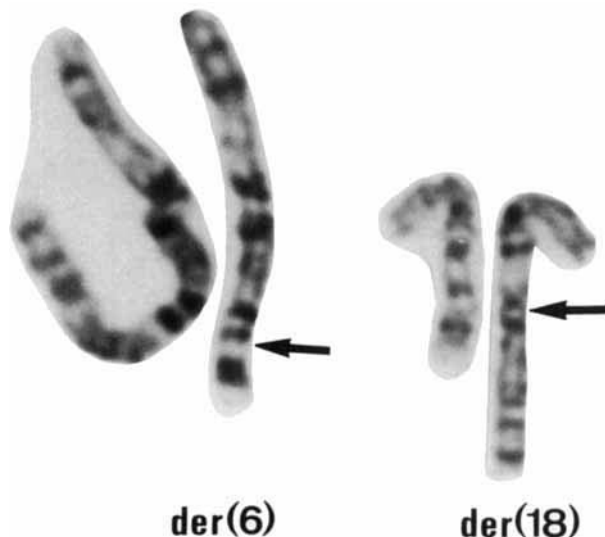


Fig. 2. Partial idiogram of the patient. Arrows show breakpoints.

To 6q21-q23.2 that is at or near one breakpoint in our patient, the human connexin43 gene (*GJA1*) was assigned [Corcos et al., 1993]. The gene product, connexin43, is one of the connexin proteins which make up the intercellular membrane channels of gap junctions. Recently, the connexin43-gene knock-out mouse was made [Reaume et al., 1995], and the null mutation of the gene resulted in neonatal death due to a swelling and blockage of the right ventricular outflow tract from the heart. The anomalies in this mutant mouse resemble congenital pulmonary stenosis in humans. In fact, *GJA1* mutations have been identified in 7 of 30 patients with a variety of congenital heart diseases, such as asplenia-polysplenia, atrial or bronchopulmonary isomerism, and familial ASD [Britz-Cunningham et al., 1993, 1995]. Although our patient had no obvious structural heart anomalies, it remains to be seen whether there is a *GJA1* mutation in our patient. Other genes mapped so far at around the region 6q21 include those for the α -chain of chorionic gonadotropin (*CGA*), α 1-chain of type X collagen (*COL10A1*) and for myristoylated alanine-rich protein kinase C substrate (*MARCKS*), and the FYN tyrosine kinase proto-oncogene (*FYN*). Although these genes have not been reported to be a cause of the heterotaxia, they may be related to the expression of other phenotypes in our patient.

Two loci, *Iv* and *Inv*, that contribute to situs abnormalities in the mouse have been identified [Brueckner et al., 1989; Yokoyama et al., 1993]. *Iv* lies on mouse chromosome 12 and is tightly linked to the mouse immunoglobulin heavy chain gene (*Igh*) cluster [Brueckner et al., 1989; Hanzlik et al., 1990]. Chromosomal localization (14q32) of human *IGH* [Nakamura et al., 1989] does not correspond to any of the breakpoints in our patient. The other locus in the mouse, *Inv*, is located to mouse chromosome 4 between the two genes, *Tsha* and *Hxb*, whose human homologs have been assigned to 6q14-q21 and 9q32-q34, respectively [Yokoyama et al., 1993]. Therefore, it is also less likely that the hypothetical human *INV* contributes to the heterotaxia in our patient.

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